

638 NUFEDWMSNPDLMLAKBAPADWGTENSGGSGSPTSTPENTALEK 690
 Db 310 NUFEDWMSNPDLMLAKBAPADWGTENSGGSGSPTSTPENTALEK 690

RESULT 2
 US-11-293-697-4145
 : Sequence 4145, Application US/11293697
 : Sequence ID No. US/000005176A
 : GENERAL INFORMATION
 : APPLICANT: HELIX RESEARCH INSTITUTE
 : TITLE OF INVENTION: Novel full length cDNA
 : CURRENT APPLICATION NUMBER: US/11/293,697
 : CURRENT FILING DATE: 2005-12-05
 : PRIOR FILING DATE: 2002-03-28
 : NUMBER OF SEQ ID NOS: 5458
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1: 5458
 : LENGTH: 620

ORGANISM: Homo sapiens
 TYPE: PRT
 11-293-697-4145

Query Match 12.11; Score 522.5; DB 7; Length 620;
 Best Local Similarity 21.11; Pred. No. 3.26; E-Value 1.0e-114;
 Matches 151; Conservative 108; Mismatches 318; Indels 49; Gaps 6;

99 ITTETPDTQGVNPNHREISGLDQGLLQKAPVPIARVTSQWFOHDEK 158
 Db 24 LKNTFCTQGLAASVGLQIRL-GPOFTGSLSSKLLPEVREHREPTLQKHP 82

159 KRNRELPNPNVGLVIRKALYEQPFRVNTISQVLTLSVDYDELQNSLP- 215
 Db 83 RNQPTFCVAGDGRLEWSSIKSENGHCIGSLATGTLTTSQRETLALDCTEL 142

216 GTTASGALVLTCTQFLLHLPVARYVYVMTDADQDQVAVLQICINQIPE 275
 Db 143 QNTQDEPSSLVNYSFLLQHPFRHLCPSATKQAKHMLAGLQICVQIQR 202

276 DSKVGFATLALVWFSQSLVGTNMLCSHVELSLWELGPELALQPLKCK 335
 Db 203 SQAAPALVLLVLYLQHQGFQDQDQDQDQDQDQDQDQDQDQDQDQ 262

336 PQSQRCHQIQIDNIVHYETDANARFEVLYQVQANQVNTIDQITTSKSLA 395
 Db 263 GRASAMETLNVHANVLAGSAGLQQLQPEQKQELASGLKSTFQVQAGVAV 322

395 SKTRAFPLPAEVCTVQVPTPISLILQVQVQVQVQVQVQVQVQVQVQ 413
 Db 323 QRLKTLTPQDSCSLQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 382

456 GIDKGTQKESLHATVQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 543
 Db 383 SQTLEVYVSPQMDQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 512

514 EQMVAQNTVTLQQLQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 573
 Db 443 QVADQVATLQALQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 502

574 ISPELLKALQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 633
 Db 574 ISPELLKALQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 602

614 QKRNKLVKRNKMSNDVLLAKADPQW---GEYSSGGSGSGSPSTSLAS 689
 Db 563 ANDVCTSLGCL---EYPMQKQAGDSTEAERBSGACPTQPSQAA--- 604

695 KRRKAKGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 720
 Db 695 KRRKAKGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 714

RESULT 3
 US-10-445-902-39758
 : Sequence 39758, Application US/0449902
 : Sequence ID No. US/00060121958A1
 : GENERAL INFORMATION
 : APPLICANT: National Institute of Biomedical Sciences
 : TITLE OF INVENTION: Novel full length cDNA
 : CURRENT APPLICATION NUMBER: US/10/449,902
 : CURRENT FILING DATE: 2005-05-10
 : PRIOR FILING DATE: 2002-05-30
 : PRIOR APPLICATION NUMBER: JP 2002-201269
 : NUMBER OF SEQ ID NOS: 11
 : NUMBER OF SEQ ID NOS: 56791
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1: 39758
 : LENGTH: 547

ORGANISM: Oryza sativa
 TYPE: PRT
 10-449-902-39758

Query Match 5.24; Score 225; DB 6; Length 547;
 Best Local Similarity 21.11; Pred. No. 3.26; E-Value 1.0e-114;
 Matches 121; Conservative 105; Mismatches 235; Indels 112; Gaps 24;

98 KLTFEFTQFTQDQVAPLN-SMHEHETGTFQMLQKLVPL----DERVYSGPL 151
 Db 20 KFLZFNKYSMLVNVAKVATLQDVAAGTGNEL--KCPKEDPAQK---TGMH 74

152 QHDSQKRNREFLVPHITGLVFNKATCTGVPRVYVNAQVILTEV-PTYLELI 210
 Db 75 KESLILQKNGFTVFGKMLVDTNTEQDQKAGKGTGLNSMRITRQPTVTKLI 134

211 GNSLPATKSSSRLAKCTQFPLHLPVARYVYVMTDADQDQVAVLQICIN 269
 Db 135 LDALCNLVQDLPKPEVLPQFELHIEB-TBTLVLCNADNDSHMOILDQD-RVY 192

270 NQGLP-ESKVGKQATATKTYQKQKLTCTHMLQCNVQVQVQVQVQVQVQ 325
 Db 193 SGLGNTSDKLTNQLFQWALVRSRQKQVYSSGSGSQQYITDCTHVAVWPSD 252

325 ALZCLPQKAPQDQ------QKQKQISDAVHYVHYVQKARFVLSQV 370
 Db 252 ALZCLPQKAPQDQ------QKQKQISDAVHYVHYVQKARFVLSQV 370

371 QVDPANQVITDQMLQITSSKELAKIVTLPAEVCTVQVQVQVQVQVQVQ 311
 Db 371 QVDPANQVITDQMLQITSSKELAKIVTLPAEVCTVQVQVQVQVQVQVQ 311

312 DQVQ 353
 Db 312 DQVQ 353

431 QGTEVQV 479
 Db 431 QGTEVQV 479

480 CTYERSESLGQKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 533
 Db 480 CTYERSESLGQKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 533

413 VFSVQSGKQDQ------KABRLKLTANLFTFTLEBAGNHQRI 457
 Db 413 VFSVQSGKQDQ------KABRLKLTANLFTFTLEBAGNHQRI 457

534 -GPEKEL--CK-SIQVLRVPL--KATDIDSSSVKPFRRFALLQITPFLKAP 585
 Db 534 -GPEKEL--CK-SIQVLRVPL--KATDIDSSSVKPFRRFALLQITPFLKAP 585

459 ASSTNLTALQKASQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 618
 Db 459 ASSTNLTALQKASQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 618

586 TCKSGLPQVLLPFLPQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 618
 Db 586 TCKSGLPQVLLPFLPQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQ 618

518 P-----ED-----ILKTNILQ 532
 Db 518 P-----ED-----ILKTNILQ 532

RESULT 4
 BS-11-289-102-117

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: Jun 24, 2006, 01:56:30 ; Search time 38.7072 Seconds
1856.571 Million call updates/sec
(without alignments)

Title: US-10-612-318-2
Perfect score: 4313
Sequence: 1 MEVQVHGLKPLAGL.....SHFAFTTDSAGVTF 821

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
2: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
3: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
4: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
5: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
6: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*
7: /BNC Colerra_S1D83/prodata/2/ias/a_COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the best score found. Printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	176.5	3.1	2030	US-09-538-092-1081
2	176.5	3.1	2120	US-09-538-092-1081
3	155.5	3.7	1248	US-09-090-497-2
4	155.5	3.7	1315	US-08-899-595-3
5	155.5	3.7	1315	US-08-899-595-3
6	152.5	3.5	864	US-09-538-092-1268
7	151.5	3.5	1255	US-09-538-092-1268
8	151.5	3.5	1255	US-09-538-092-1268
9	151.5	3.5	1255	US-09-538-092-1268
10	147.5	3.4	688	US-09-141-041-8
11	147.5	3.4	688	US-09-141-041-8
12	147.5	3.4	688	US-09-141-041-8
13	146.5	3.4	693	US-09-081-385-154
14	146.5	3.4	693	US-09-081-385-154
15	146.5	3.4	693	US-09-081-385-154
16	146.5	3.4	693	US-09-081-385-154
17	144.5	3.3	983	US-09-700-354-154
18	144.5	3.3	983	US-09-700-354-154
19	144.5	3.3	983	US-09-700-354-154
20	143.5	3.3	916	US-09-092-546-16777
21	142.5	3.3	916	US-09-092-546-16777
22	142.5	3.3	916	US-09-092-546-16777
23	142.5	3.3	916	US-09-092-546-16777
24	139.5	3.2	638	US-09-538-092-1081
25	137.5	3.2	912	US-09-090-497-2
26	137.5	3.2	912	US-09-090-497-2

ALIGNMENTS

RESULT 1

Sequence 1081, Application US/09538092

Sequence 1081, Application US/09538092

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Sequence 1081, Application US/09538092

Sequence 1081, Application US/09538092

Genome version 5.1.9
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ON protein - protein search, using sw model

Run on: June 24, 2006, 01:50:05 ; Search time 31.0676 Seconds
(without alignments)
2542.46 Million cell updates/sec

Title: US-10-612-318-2
Perfect score: 4313
Sequence: 1 MEEVGQRMGKPLAGLGG.....SSHPAHTTDSAGVTSF 821

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 203416 seqs, 9516763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p100*
2: p101*
3: p102*
4: p103*

Pred. No. is the number of results predicted by chance to have a
score at least as good as the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3224	84.0	696	2	746394	hypothetical prote
2	1752	2090	2	926558		probable transform
3	1622	888	2	915762		hypothetical prote
4	1616	888	2	915762		hypothetical prote
5	1616	888	2	915762		hypothetical prote
6	152.5	3.5	1087	1	QF0SH	neurofilament trip
7	151.1	3.5	1087	1	QF0SH	neurofilament trip
8	151.1	3.5	1087	1	QF0SH	neurofilament trip
9	148.4	3.4	1017	2	PC035	diaphanous protein
10	147.4	3.4	990	2	714756	cali-cytle-depende
11	146.5	3.4	990	2	714756	cali-cytle-depende
12	146.5	3.4	990	2	714756	cali-cytle-depende
13	146.5	3.4	802	2	943382	elastic titin - bu
14	146.5	3.4	802	2	943382	elastic titin - bu
15	146.5	3.4	802	2	943382	elastic titin - bu
16	145.8	3.4	1018	2	741368	hypothetical prote
17	145.8	3.4	1018	2	741368	hypothetical prote
18	145.8	3.4	1018	2	741368	hypothetical prote
19	145.8	3.4	1018	2	741368	hypothetical prote
20	143.5	3.3	1261	1	TVTM20	neurofilament trip
21	143.5	3.3	1261	1	TVTM20	neurofilament trip
22	143.5	3.3	1261	1	TVTM20	neurofilament trip
23	142.5	3.3	802	2	943382	neurofilament trip
24	142.5	3.3	802	2	943382	neurofilament trip
25	141.1	3.2	1020	1	QF0SH	neurofilament trip
26	141.1	3.2	1020	1	QF0SH	neurofilament trip
27	138.5	3.2	2568	2	823236	calcium channel pr
28	138.5	3.2	2568	2	823236	calcium channel pr
29	138.5	3.2	1382	2	874245	8p/sem-like transp
30	137.5	3.2	418	2	719800	hypothetical prote
31	137.5	3.2	912	2	854223	hypothetical prote
32	137.5	3.2	912	2	854223	hypothetical prote
33	137.5	3.2	912	2	854223	hypothetical prote
34	134.5	3.1	851	2	811508	Basoon protein - p
35	134.5	3.1	851	2	811508	Basoon protein - p
36	134.5	3.1	851	2	811508	Basoon protein - p
37	134.5	3.1	851	2	811508	Basoon protein - p
38	133.5	3.1	1234	2	700363	probable transcrip
39	133.5	3.1	1234	2	700363	probable transcrip
40	133.5	3.1	1234	2	700363	probable transcrip
41	132.5	3.1	1827	2	716700	diaphanous protein
42	132.5	3.1	1827	2	716700	diaphanous protein
43	132.5	3.1	1827	2	716700	diaphanous protein
44	132.5	3.1	1827	2	716700	diaphanous protein
45	131.5	3.0	885	2	702225	serine/threonine-s

ALIGNMENTS

RESULT 1

746394

hypothetical protein DNFZM34H0920.1 - human (fragment)

CDate: 04-Feb-2006

Sequence revision 04-Feb-2006

Accession: 746394

Accession: 746394

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RefSeq No.	Score	Query Match	Length	DB ID	Description
2	4111	100.0	821	ADL23466	Adi23466 Human STR
2	4114	95.4	821	ADL23468	Adi23468 Human STR
3	3399	88.1	733	AD055194	AD055194 Protein #
4	3391	87.9	736	AD051275	AD051275 Protein #
5	3388	87.9	733	AD051275	AD051275 Protein #
6	3362	84.9	733	AB111456	AB111456 Human Mgi
7	3687	81.7	733	ABP62233	ABP62233 Human pol
8	2227	47.0	356	AB054433	AB054433 Human pol
9	2227	47.0	356	AB054433	AB054433 Human pol
10	1164	27.0	928	AB943043	AB943043 Junao ac1
11	1164	27.0	928	ADY17213	ADY17213 PRO poly p
12	1164	27.0	928	ADY17213	ADY17213 PRO poly p
13	1164	27.0	928	ADY17213	ADY17213 PRO poly p
14	1164	27.0	928	ADY17213	ADY17213 PRO poly p
15	1164	27.0	928	ADY17213	ADY17213 PRO poly p
16	1160	26.9	928	ADY17213	ADY17213 PRO poly p
17	9815	25.6	726	ADY17213	ADY17213 PRO poly p
18	9815	25.6	726	ADY17213	ADY17213 PRO poly p
19	9257	19.2	383	AD044921	AD044921 Cancer -as
20	658	5.5	383	AD044921	AD044921 Cancer -as
21	658	5.5	383	AD044921	AD044921 Cancer -as
22	432	12.6	703	AB042734	AB042734 Human GSP
23	432	12.6	703	AB042734	AB042734 Human GSP
24	432	12.6	703	AB042734	AB042734 Human GSP
25	432	12.6	703	AB042734	AB042734 Human GSP
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59	432	12.6	703	AB042734	AB042734 Human GSP
60	432	12.6	703	AB042734	AB042734 Human GSP
61	432	12.6	703	AB042734	AB042734 Human GSP
62	432	12.6	703	AB042734	AB042734 Human GSP

Result No.	Score	Query Length	DB ID	Description
1	355.4	78.4	3656	AL137555 Mus musc
2	288.4	48.2	2186	AL055555 Homo sapi
3	175.55	36.7	3656	AL055555 Homo sapi
4	175.55	36.7	3656	AL153489 Mus musc
5	172.5	38.7	3590	AK046893 Mus musc
6	172.5	38.7	3631	AK105942 Mus musc
7	172.5	38.7	3631	AK105942 Mus musc
8	172.5	38.7	3631	AK152307 Mus musc
9	172.5	38.7	3631	AK152307 Mus musc
10	172.5	38.7	3631	AK152307 Mus musc
11	172.5	38.7	3631	AK152307 Mus musc
12	172.5	38.7	3631	AK152307 Mus musc
13	172.5	38.7	3631	AK152307 Mus musc
14	168.2	2.2	985	AL055555 Homo sapi
15	168.2	2.2	985	AL055555 Homo sapi
16	168.2	2.2	985	AL055555 Homo sapi
17	833.6	13.4	928	BC039370 HOMO SAPI
18	833.6	13.4	928	BC039370 HOMO SAPI
19	833.6	13.4	928	BC039370 HOMO SAPI
20	833.6	13.4	928	BC039370 HOMO SAPI
21	833.6	13.4	928	BC039370 HOMO SAPI
22	833.6	13.4	928	BC039370 HOMO SAPI
23	833.6	13.4	928	BC039370 HOMO SAPI
24	833.6	13.4	928	BC039370 HOMO SAPI
25	833.6	13.4	928	BC039370 HOMO SAPI
26	833.6	13.4	928	BC039370 HOMO SAPI
27	833.6	13.4	928	BC039370 HOMO SAPI
28	833.6	13.4	928	BC039370 HOMO SAPI
29	833.6	13.4	928	BC039370 HOMO SAPI
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69	827.5	19.8	748	2	OSVPRC_MOUSE
70	827.5	19.8	748	2	OSVPRC_MOUSE
71	827.5	19.8	748	2	OSVPRC_MOUSE
72	827.5	19.8	748	2	OSVPRC_MOUSE
73	827.5	19.8	748	2	OSVPRC_MOUSE
74	827.5	19.8	748	2	OSVPRC_MOUSE
75	827.5	19.8	748	2	OSVPRC_MOUSE</

BL Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135 (2004).

CC -1- SIMILARITY: belongs to the Niiban family.

CC -2- SIMILARITY: Conserved.

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CC

DR ENBL; AF151783; AKS7556.1; -, rRNA.

DR ENBL; AL137555; CAP7089.1; -, rRNA.

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DR ENBL; AF151783; AKS7556.1; -, rRNA.

DR ENBL; AF151783; AKS7556.1; -, rRNA.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Result	Score	Query Length	DB ID	Description
1	100	100	821	8	AD124668 Human STR
2	114	99.4	821	8	AD123468
3	384	92.4	733	8	ADG55194 Protein #
4	383	92.3	733	8	ADG55194
5	383	92.3	733	8	ADH11566
6	383	92.3	733	8	ADH11566
7	372	91.5	746	8	ADG91075 Tumor-ns
8	372	91.5	746	8	ADG91075 Human pool
9	372	91.5	746	8	ADG91075
10	372	91.5	746	8	ADG91075
11	1160	98.9	928	9	ADT17113 Human pro
12	1160	98.9	928	9	ADT17113 Human pro
13	1160	98.9	928	9	ADT17113 PRO polyP
14	1160	98.9	928	9	ADT17113 PRO polyP
15	1160	98.9	928	9	ADT17113 PRO polyP
16	1136	97.9	928	9	ADG07465 Cancer-as
17	985.5	23.9	246	8	ADG10972 Human acc
18	985.5	23.9	246	8	ADG10972 Human acc
19	985.5	23.9	246	8	ADG10972 Human acc
20	985.5	23.9	246	8	ADG10972 Human acc
21	985.5	23.9	246	8	ADG10972 Human acc
22	985.5	23.9	246	8	ADG10972 Human acc
23	985.5	23.9	246	8	ADG10972 Human acc
24	985.5	23.9	246	8	ADG10972 Human acc
25	985.5	23.9	246	8	ADG10972 Human acc
26	985.5	23.9	246	8	ADG10972 Human acc
27	985.5	23.9	246	8	ADG10972 Human acc
28	985.5	23.9	246	8	ADG10972 Human acc
29	985.5	23.9	246	8	ADG10972 Human acc
30	985.5	23.9	246	8	ADG10972 Human acc
31	985.5	23.9	246	8	ADG10972 Human acc
32	985.5	23.9	246	8	ADG10972 Human acc
33	985.5	23.9	246	8	ADG10972 Human acc
34	985.5	23.9	246	8	ADG10972 Human acc
35	985.5	23.9	246	8	ADG10972 Human acc
36	985.5	23.9	246	8	ADG10972 Human acc
37	985.5	23.9	246	8	ADG10972 Human acc
38	985.5	23.9	246	8	ADG10972 Human acc
39	985.5	23.9	246	8	ADG10972 Human acc
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60	985.5	23.9	246	8	ADG10972 Human acc
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62	985.5	23.9	246	8	ADG10972 Human acc
63	985.5	23.9	246	8	ADG10972 Human acc
64	985.5	23.9	246	8	ADG10972 Human acc
65	985.5	23.9	246	8	ADG10972 Human acc
66	985.5	23.9	246	8	ADG10972 Human acc
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69	985.5	23.9	246	8	ADG10972 Human acc
70	985.5	23.9	246	8	ADG10972 Human acc
71	985.5	23.9	246	8	ADG10972 Human acc
72	985.5	23.9	246	8	ADG10972 Human acc
73	985.5	23.9	246	8	ADG10972 Human acc
74	985.5	23.9	246	8	ADG10972 Human acc
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77	985.5	23.9	246	8	ADG10972 Human acc
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80	985.5	23.9	246	8	ADG10972 Human acc
81	985.5	23.9	246	8	ADG10972 Human acc
82	985.5	23.9	246	8	ADG10972 Human acc
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84	985.5	23.9	246	8	ADG10972 Human acc
85	985.5	23.9	246	8	ADG10972 Human acc
86	985.5	23.9	246	8	ADG10972 Human acc
87	985.5	23.9	246	8	ADG10972 Human acc
88	985.5	23.9	246	8	ADG10972 Human acc
89	985.5	23.9	246	8	ADG10972 Human acc
90	985.5	23.9	246	8	ADG10972 Human acc
91	985.5	23.9	246	8	ADG10972 Human acc
92	985.5	23.9	246	8	ADG10972 Human acc
93	985.5	23.9	246	8	ADG10972 Human acc
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95	985.5	23.9	246	8	ADG10972 Human acc
96	985.5	23.9	246	8	ADG10972 Human acc
97	985.5	23.9	246	8	ADG10972 Human acc
98	985.5	23.9	246	8	ADG10972 Human acc
99	985.5	23.9	246	8	ADG10972 Human acc
100	985.5	23.9	246	8	ADG10972 Human acc

ALIGNMENTS

RESULT 1
ADL23468
ID ADL23468 standard; protein; 791 AA

AC
XX
ADL23468:

01--III--2004 (first entry)

XXI

XX
XX

neurodegenerative disease; stroke; Parkinson's disease

Alzheimers Disease; naming; antiparacerebroprotective; vasotropic; antipar

nootropic; anticonvulsant.

Homo sapiens.

PN US2004068098-A1.

PD 08-APR-2004.

01-JUL-2003; 2003US-00612318.

XX
00 01 JAN 2003 2002718-0293251P

1998

PA (FAER/) FABRMAN A.

FA (FBI) / FBI OK 2 :
XX

XX
PI
KASHCHATSKY SG, RABINMAN N, FELD-OT 21

DR: 2004-304622/2B.
M-PCPB: 2004-304622/2B.
M-PCPB: 2004-304622/2B.

XX

PT treating neurodegenerative diseases,

[illegible]

PS CLAIM 15; SEQ ID NO 4; 38pp; English.
XX

The invention relates to a purified poly-
amino-acetate. The purified poly-

CC to modulate neurotoxic stress. The po

neurodegenerative diseases, e.g. stroke

